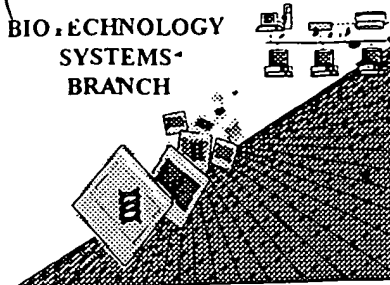


015
1011

BIO. TECHNOLOGY
SYSTEMS-
BRANCH

J

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/584411

Source: O I P E

Date Processed by STIC: 09/10/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/584,411

TIME: 09:12:56

Input Set : A:\Cura521.app

Output Set: N:\CRF3\09102001\I584411.raw

5 <110> APPLICANT: Shimkets et al
 9 <120> TITLE OF INVENTION: Novel polynucleotides and polypeptides encoded thereby
 13 <130> FILE REFERENCE: 15966-552
 17 <140> CURRENT APPLICATION NUMBER: 09/584,411
 C--> 19 <141> CURRENT FILING DATE: 2001-08-21
 23 <150> PRIOR APPLICATION NUMBER: USSN 60/137,322
 25 <151> PRIOR FILING DATE: 1999-06-03
 28 <150> PRIOR APPLICATION NUMBER: USSN 60/189,810
 30 <151> PRIOR FILING DATE: 2000-03-16
 33 <150> PRIOR APPLICATION NUMBER: USSN 60/191,158
 35 <151> PRIOR FILING DATE: 2000-03-22
 38 <150> PRIOR APPLICATION NUMBER: USSN 60/193,086
 40 <151> PRIOR FILING DATE: 2000-03-30
 43 <150> PRIOR APPLICATION NUMBER: USSN 60/201,388
 45 <151> PRIOR FILING DATE: 2000-05-03
 49 <160> NUMBER OF SEQ ID NOS: 93
 53 <170> SOFTWARE: PatentIn Ver. 2.0
 57 <210> SEQ ID NO: 1
 59 <211> LENGTH: 836
 61 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 67 <220> FEATURE:
 69 <221> NAME/KEY: CDS
 71 <222> LOCATION: (189)..(695)
 75 <220> FEATURE:
 77 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
 79
 83 <400> SEQUENCE: 1
 85 cagagtccct acccttttga gaactgcgct tctcttttcgg agggagtgtt cgccgcccgc 60
 89 gcggcccgcca cctggagttt cttcagactc cagattttccc tgtcaaccac gaggagtcca 120
 93 gagaggaaac gcggagcgga gacaacagta cctgacgcct ctttcagccc gggatcgccc 180
 97 cagcaggg atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg 230
 99 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu
 101 1 5 10
 105 gcc gct ctg ctt cgg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct 278
 107 Ala Ala Leu Leu Arg Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro
 109 15 20 25 30
 113 tcc ctc gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag 326
 115 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu
 117 35 40 45
 121 tgc ttc tac cag ccc atg ccc ctg aag gcc tcg ctg gag atc gag tac 374
 123 Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr
 125 50 55 60
 129 caa gtt tta gat gga gca gga tta gat att gat ttc cat ctt acc tct 422
 131 Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Thr Ser
 133 65 70 75
 137 cca gaa ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt 470

Does Not Comply
 Corrected Diskette Needed

See pages
 2 of 7 and 3 of 7

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/584,411

TIME: 09:12:56

Input Set : A:\Cura521.app

Output Set: N:\CRF3\09102001\I584411.raw

```

139 Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val
141      80                      85                      90
145 cac act gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat 518
147 His Thr Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn
149 95                      100                      105                      110
153 aca ttc agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg 566
155 Thr Phe Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu
157                      115                      120                      125
161 gat aat atg gga gaa cag gca caa gaa gaa gat tgg aag aaa tat 614
163 Asp Asn Met Gly Glu Gln Ala Gln Glu Glu Asp Trp Lys Lys Tyr
165                      130                      135                      140
169 att act ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gac 662
171 Ile Thr Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Asp
173                      145                      150                      155
177 ctg ccc ggg cgg ccg ctc gag ccc tat agt gag taagtctgga ggccccggg 715
179 Leu Pro Gly Arg Pro Leu Glu Pro Tyr Ser Glu
181 160                      165
185 gccgctcctg cagtagggta ccgagctcgt cgacgcatgc tgatctagat ctttaattaac 775
189 acgtggtgcc aagctttgga agactcagct tttgttcctt ttagtgaggg ttaatttcga 835
193 g 836
199 <210> SEQ ID NO: 2
201 <211> LENGTH: 169
203 <212> TYPE: PRT
205 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
211 <221> NAME/KEY: variant
213 <222> LOCATION: (1)..(169)
215 <223> OTHER INFORMATION: where Xaa can any amino acid
219 <400> SEQUENCE: 2
221 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
223 1 5 10 15
227 Leu Leu Arg Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
229 20 25 30
233 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
235 35 40 45
239 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
241 50 55 60
245 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Thr Ser Pro Glu
247 65 70 75 80
251 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
253 85 90 95
257 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
259 100 105 110
263 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
265 115 120 125
269 Met Gly Glu Gln Ala Gln Glu Glu Asp Trp Lys Lys Tyr Ile Thr
271 130 135 140
275 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Asp Leu Pro
277 145 150 155 160

```

Errored

OK

However, according to the Rules you must enumerate all unknowns in the sequence listing

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/584,411

DATE: 09/10/2001

TIME: 09:12:56

Input Set : A:\Cura521.app

Output Set: N:\CRF3\09102001\I584411.raw

281 Gly Arg Pro Leu Glu Pro Tyr Ser Glu
 283 165
 289 <210> SEQ ID NO: 3
 291 <211> LENGTH: 2342
 293 <212> TYPE: DNA
 295 <213> ORGANISM: Homo sapiens
 299 <220> FEATURE:
 301 <221> NAME/KEY: CDS
 303 <222> LOCATION: (110)..(1750)
 307 <220> FEATURE:
 309 <221> NAME/KEY: variation
 311 <222> LOCATION: (1)..(711)
 313 <223> OTHER INFORMATION: where n can be any nucleotide
 317 <400> SEQUENCE: 3
 319 agacccgctg agctgctagc ccgccggcca gcgagtgaga ggtcggacag actgtggagc 60
 323 cgacagactg aaggacagcg gcaccgccag acggccagaa agttccgcc atg agc tgg 118
 325 Met Ser Trp
 327 1
 331 ggc acg gag ctg tgg gat cag ttc gac agc tta gac aag cat aca caa 166
 333 Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys His Thr Gln
 335 5 10 15
 339 tgg gga att gac ttc ttg gaa aga tat gcc aaa ttt gtt aaa gag agg 214
 341 Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val Lys Glu Arg
 343 20 25 30 35
 347 ata gaa att gaa cag aac tat gcg aaa caa ttg aga aat ctg gtt aag 262
 349 Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn Leu Val Lys
 351 40 45 50
 355 aag tac tgc ccc aaa cgt tca tcc aaa gat gaa gag cca cgg ttt acc 310
 357 Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro Arg Phe Thr
 359 55 60 65
 363 tcg tgt gta gcc ttt ttt aat atc ctt aat gag tta aat gac tat gca 358
 365 Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn Asp Tyr Ala
 367 70 75 80
 371 gga cag cga gaa gtt gta gca gaa gaa atg gcg cac aga gtg tat ggt 406
 373 Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg Val Tyr Gly
 375 85 90 95
 379 gaa tta atg aga cat gct cat gat ctg aaa act gaa aga aaa atg cat 454
 381 Glu Leu Met Arg His Ala His Asp Leu Lys Thr Glu Arg Lys Met His
 383 100 105 110 115
 387 ctg caa gaa ggc cga aaa gct cac caa tct ctt gcc atg tgc tgg aac 502
 389 Leu Gln Glu Gly Arg Lys Ala His Gln Ser Leu Ala Met Cys Trp Asn
 391 120 125 130
 395 cag atg gat aat agt aaa aag aag ttt gaa aga gaa tgt aga gag gca 550
 397 Gln Met Asp Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys Arg Glu Ala
 399 135 140 145
 403 gaa aag gcc cac cag agt tat gaa aga ttg gat aat gat act aat gca 598
 405 Glu Lys Ala His Gln Ser Tyr Glu Arg Leu Asp Asn Asp Thr Asn Ala
 407 150 155 160
 411 acc aag gca gat gtt gaa aat gcc aaa cag cag ttg aat ctg cgt acg 646

*must drop
 Errored:
 Field 222 does not include
 all unknowns in the DNA
 sequence. looking*

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/584,411

TIME: 09:12:56

Input Set : A:\Cura521.app

Output Set: N:\CRF3\09102001\I584411.raw

```

413 Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn Leu Arg Thr
415      165      170      175
419 cat atg gcc gat gaa aat aaa aat gca tat gct gca caa tta caa aac 694
421 His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln Leu Gln Asn
423 180      185      190      195
427 ttt aat gga gaa caa cat aaa cat ttt tat gta gtg att cct cag att 742
429 Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile Pro Gln Ile
431      200      205      210
435 tac aag caa cta caa gaa atg gac gaa cga agg act att aaa ctc agt 790
437 Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile Lys Leu Ser
439      215      220      225
443 gag tgt tac aga gga ttt gct gac tca gaa cgc aaa gtt att ccc atc 838
445 Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile Pro Ile
447      230      235      240
451 att tca aaa tgt ttg gaa gga atg att ctt gca gca aaa tca gtt gat 886
453 Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser Val Asp
455      245      250      255
459 gaa aga aga gac tct caa atg gtg gta gac tcc ttc aaa tct ggt ttt 934
461 Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser Gly Phe
463 260      265      270      275
467 gaa cct cca gga gac ttt cca ttt gaa gat tac agt caa cat ata tat 982
469 Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr
471      280      285      290
475 aga acc att tct gat ggg act atc agt gca tcc aaa cag gag agt ggg 1030
477 Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly
479      295      300      305
483 aag atg gat gcc aaa acc cca gta gga aag gcc aag ggc aaa ttg tgg 1078
485 Lys Met Asp Ala Lys Thr Pro Val Gly Lys Ala Lys Gly Lys Leu Trp
487      310      315      320
491 ctc ttt gga aag aag cca aag ggc cca gca cta gaa gat ttc agt cat 1126
493 Leu Phe Gly Lys Lys Pro Lys Gly Pro Ala Leu Glu Asp Phe Ser His
495      325      330      335
499 ctg cca cca gaa cag aga cgt aaa aaa cta cag cag cgc att gat gaa 1174
501 Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu
503 340      345      350      355
507 ctt aac aga gaa cta cag aaa gaa tca gac caa aaa gat gca ctc aac 1222
509 Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn
511      360      365      370
515 aaa atg aaa gat gta tat gag aag gat cca caa atg ggg gat cca ggg 1270
517 Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly Asp Pro Gly
519      375      380      385
523 agt ttg cag cct aaa tta gca gag acc atg aat aac att gac cgc cta 1318
525 Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile Asp Arg Leu
527      390      395      400
531 cga atg gaa atc cat aag aat gag gct tgg ctc tct gaa gtc gaa ggc 1366
533 Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu Val Glu Gly
535      405      410      415
539 aaa aca ggt ggg aga gga gac aga aga cat agc agt gac ata aat cat 1414
541 Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp Ile Asn His

```

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/584,411

TIME: 09:12:56

Input Set : A:\Cura521.app

Output Set: N:\CRF3\09102001\I584411.raw

```

543 420          425          430          435
547 ctt gta aca cag gga cga gaa agt cct gag gga agt tac act gat gat 1462
549 Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp
551          440          445          450
555 gca aac cag gaa gtc cgt ggg cca ccc cag cag cat ggt cac cac aat 1510
557 Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly His His Asn
559          455          460          465
563 gag ttt gat gat gaa ttt gag gat gat gat ccc ttg cct gct att gga 1558
565 Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly
567          470          475          480
571 cac tgc aaa gct atc tac cct ttt gat gga cat aat gaa ggt act cta 1606
573 His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu Gly Thr Leu
575          485          490          495
579 gca atg aaa gaa ggt gaa gtt ctc tac att ata gag gag gac aaa ggt 1654
581 Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly
583 500          505          510          515
587 gac gga tgg aca aga gct cgg aga cag aac ggt gaa gaa ggc tac gtt 1702
589 Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val
591          520          525          530
595 ccc acg tca tac ata gat gta act cta gag aaa aac agt aaa ggt tcc 1750
597 Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ser
599          535          540          545
603 tgaagaggggt ttctgaggaa atgggcaaga tggtgaagga gggtacatgc agctgctttt 1810
607 ggggggaggggt attagagttg tcaggctcaa agagagtgag agaagcaagt tgcagtagtg 1870
611 catgcagaca tgattttttt ttactaact tcattagcat ttccatacat tgttttttaa 1930
615 aatcataata ccaaccctta agttcctagt tcacagttat tcccacaaaa gaaaaagcca 1990
619 acaatagtgt accattttttc tattttatatt tattgtctgtc taatcaataa agaatgcaga 2050
623 gctgtcaaaa aatgtgtcttt acatttagct gtcccaacag gattgtcttc cctccagct 2110
627 ctgggttttaa ttggctttta gaccactat ctgtcagatc cttgccatct gtcagtgtct 2170
W--> 631 gcctgcgcca cctccgtgct tgcctaacat cctgttgcat gtctagcgtg attgagcnag 2230
W--> 635 attttcaggc atgtcttttag aatccccctgg tncgtgcaaa gcctgggttg gtttacattg 2290
W--> 639 gtngtgcaat cncctttgtca acatctccag cactatngtt cctctctagg tn 2342
645 <210> SEQ ID NO: 4
647 <211> LENGTH: 547
649 <212> TYPE: PRT
651 <213> ORGANISM: Homo sapiens
655 <400> SEQUENCE: 4
657 Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys
659 1          5          10          15
663 His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val
665          20          25          30
669 Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn
671          35          40          45
675 Leu Val Lys Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro
677          50          55          60
681 Arg Phe Thr Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn
683 65          70          75          80
687 Asp Tyr Ala Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg
689          85          90          95

```

must be
described in
Field 222

VERIFICATION SUMMARY

DATE: 09/10/2001

PATENT APPLICATION: US/09/584,411

TIME: 09:12:57

Input Set : A:\Cura521.app

Output Set: N:\CRF3\09102001\I584411.raw

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:2295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:3859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:5903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:5905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:5987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:9117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/584411

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 2 & 3 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.